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1600

RAW SEQUENCE LISTING

DATE: 07/09/2003

PATENT APPLICATION: US/10/042,417A

TIME: 09:07:02

Input Set : N:\EBONY'S\042417A.txt

Output Set: N:\CRF4\07092003\J042417A.raw

3 <110> APPLICANT: Pagano, M.
 5 <120> TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
 PROLIFERATIVE
 6 AND DIFFERENTIATIVE DISORDERS
 8 <130> FILE REFERENCE: 5914-090-999
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/042,417A
 11 <141> CURRENT FILING DATE: 2002-01-07
 13 <150> PRIOR APPLICATION NUMBER: 60/260,179
 14 <151> PRIOR FILING DATE: 2001-01-05
 16 <160> NUMBER OF SEQ ID NOS: 92
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2151
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
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 28 tcctcagaga gagaagactg taataatggc gaacccccta ggaagataat accagagaag 180
 29 aattcactta gacagacata caacagctgt gccagactct gcttaaacca agaaacagta 240
 30 tgttttagcaa gcactgctat gaagactgag aattgtgtgg ccaaaacaaa acttgccaat 300
 31 ggcacttcca gtatgattgt gcccaagcaa cggaaactct cagcaagcta tgaaaaggaa 360
 32 aaggaactgt gtgtcaaata ctttgagcag tggtcagagt cagatcaagt ggaatttgtg 420
 33 gaacatctta tatcccaaat gtgtcattac caacatgggc acataaactc gtatcttaaa 480
 34 cctatgttgc agagagattt cataactgct ctgccagctc ggggattgga tcatatcgct 540
 35 gagaacattc tgtcatacct ggatgcaaaa tcaactatgt ctgctgaact tgtgtgcaag 600
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 37 aggacagatt ctctgtggag aggcctggca gaacgaagag gatggggaca gtatttatc 720
 38 aaaaacaaac ctccgtacgg gaatgctcct cccaactctt tttatagagc actttatcct 780
 39 aaaattatac aagacattga gacaatagaa tctaattgga gatgtggaag acatagttta 840
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56 acttgcccag gacccattaa agttgcggtta tttaacgtat ctgccaatac caggatgagc 1860
57 aacaacagta acaatcaaac tactgcccag tttccctgga ctagccgagg agcagggtt 1920
58 tgagactcct gttgggacac agttggtctg cagtcggccc aggacggtct actcagcaca 1980
59 actgactgct tcagtgtctg tatcagaaga tgtcttctat caattgtgaa tgattggaac 2040
60 ttttaaacct cccctcctct cctcctttca cctctgcacc tagttttttc ccattgggtc 2100
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75 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
76 35 40 45
78 Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
79 50 55 60
81 Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
82 65 70 75 80
84 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
85 85 90 95
87 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
89 100 105 110
91 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
92 115 120 125
94 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
95 130 135 140
97 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
98 145 150 155 160
100 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
101 165 170 175
103 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
104 180 185 190
106 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
107 195 200 205
109 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
110 210 215 220
112 Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
113 225 230 235 240
115 Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
116 245 250 255
118 Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
119 260 265 270
121 Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
122 275 280 285

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127 Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
128 305                      310                      315                      320
130 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
131                      325                      330                      335
133 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
134                      340                      345                      350
136 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
137                      355                      360                      365
139 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
140      370                      375                      380
142 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
143 385                      390                      395                      400
145 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
146                      405                      410                      415
148 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
149                      420                      425                      430
151 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
152                      435                      440                      445
154 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
155      450                      455                      460
157 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
158 465                      470                      475                      480
160 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
161                      485                      490                      495
163 Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
164                      500                      505                      510
166 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
167                      515                      520                      525
169 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
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187 ctcaggcatc tctccaataa ctagagact ctcctcaagc gggacttcct caaactcctt 180
188 cccctggagc tcagttttta tttgttaaaa tggctcgatc ctcagacttt actcacatgc 240
189 tgcctcgtct ctaaacagtg gaataaggtg ataagtgcct gtacagaggt gtggcagact 300
190 gcatgtaaaa atttgggctg gcagatagat gattctgttc aggacgcttt gactggaag 360
191 aaggtttatt tgaaggctat tttgagaatg aagcaactgg aggaccatga agcctttgaa 420
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195 acaggctcct ttgacaacac tgtggccttc tgggaatgga gttccggagc caggacccag 660
196 cactttcggg ggcacacggg ggcggtattt agcgtggact acaatgatga actggatatc 720
197 ttggtgagcg gctctgcaga cttcactgtg aaagtatggg ctttatctgc tgggacatgc 780
198 ctgaacacac tcaccgggca cacggaatgg gtcaccaagg tagttttgca gaagtgcaa 840
199 gtcaagtctc tcttgcacag tcctggagac tacatcctct taagtgcaga caaatatgag 900
200 attaagattt ggccaattgg gagagaaatc aactgtaagt gcttaaagac attgtctgtc 960
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203 atcaagactc ctgagatagc aaacttggcc ttgcttggct ttggagatat ctttgccctg 1140
204 ctgtttgaca accgctacct gtacatcatg gacttgcgga cagagagcct gattagtgcg 1200
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208 cgctgactga ctttgggtgc cggggctgcg ggttttgggt gcacctctgc ggcacgcgac 1440
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221 20 25 30
223 Ile Ser Leu Ser Gly Ala Val Gln Leu Arg His Leu Ser Asn Asn Leu
224 35 40 45
226 Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
227 50 55 60
229 Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys
230 65 70 75 80
232 Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu
233 85 90 95
235 Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp Ser
236 100 105 110
238 Val Gln Asp Ala Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile Leu
239 115 120 125
241 Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser Leu
242 130 135 140
244 Ile Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly Leu
245 145 150 155 160
247 Leu Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp Val Ser
248 165 170 175
250 Thr Gly Gln Cys Val Tyr Gly Ile Gln Thr His Thr Cys Ala Ala Val
251 180 185 190
253 Lys Phe Asp Glu Gln Lys Leu Val Thr Gly Ser Phe Asp Asn Thr Val
254 195 200 205
256 Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg Gly

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262 Leu Val Ser Gly Ser Ala Asp Phe Thr Val Lys Val Trp Ala Leu Ser
263      245      250      255
265 Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val Thr
266      260      265      270
268 Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser Pro
269      275      280      285
271 Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile Trp
272      290      295      300
275 Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser Val
276 305      310      315      320
278 Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp Gly
279      325      330      335
281 Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp Phe
282      340      345      350
284 Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Ile Ala Asn
285      355      360      365
287 Leu Ala Leu Leu Gly Phe Gly Asp Ile Phe Ala Leu Leu Phe Asp Asn
288      370      375      380
290 Arg Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser Arg
291 385      390      395      400
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308 atgagcattc tcagacttgt gattggggta atctccttca ggacattatt ctccaagtat 180
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314 ctcgaccaag ctttatggat ttaccaaagt ctcactttat ctctgcactg acagtttgtgt 540
315 tcgtaaaactc caaatccctg tcttcgctta agatagatga tactccagta gatgatccat 600
316 ctctcaaagt actagtggcc aacaatagtg atacactcaa gctgttgaaa atgagcagct 660
317 gtcctcatgt ctctccagca ggtatccttt gtgtggctga tcagtgtcac ggcttaagag 720
318 aactagccct gaactaccac ttattgagtg atgagttgtt acttgcattg tcttctgaaa 780
319 aacatgttcg attagaacat ttgcgcattg atgtagtcag tgagaatcct ggacagacac 840
320 atttccatac tattcagaag agtagctggg atgctttcat cagacattca ccaaagtga 900
321 acttagtgat gtattttttt ttatatgaag aagaatttga ccccttcttt cgctatgaaa 960
322 tacctgccac ccatctgtac tttgggagat cagtaagcaa agatgtgctt ggccgtgtgg 1020

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:29; N Pos. 13,47,68,88,270
Seq#:30; Xaa Pos. 15,22,28,89
Seq#:37; N Pos. 45,329,332
Seq#:38; Xaa Pos. 110,111
Seq#:51; N Pos. 1733
Seq#:52; Xaa Pos. 576,586
Seq#:53; N Pos. 348
Seq#:54; Xaa Pos. 150,309,340,374
Seq#:59; N Pos. 471